SEQUENCE LISTING

<110> OHARA, Osamu
      NAGASE, Takahiro
      OISHI, Michio
      YOKOTA, Hiroshi
      KAMIDA, Osamu

<120> Gene encoding a guanine nucleotide exchange factor and the gene product thereof

<130> 3190-100

<140> US Unassigned
<141> 2006-09-28

<150> PCT/JP2005/005918
<151> 2005-03-29

<150> JP P2004-106268
<151> 2004-03-31

<160> 27

<170> PatentIn version 3.1

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tccgggccag ctgaggggct ggcggtgggc gggagcggtc ggcggcctca gccccttcag     180

agagcgactt tcaaactcgc gcccgcgtcg cggcagcacc tgggcagccc cgcacgccgt     240

gcgcgtcccg agcccgcggg gcagctaccg ctcgaatctc cctggggtgc cctccccagg     300

cagcaatgcc agg atg cct gtg tcc acc tcc ctc cac cag gat ggc agc       349
            Met Pro Val Ser Thr Ser Leu His Gln Asp Gly Ser
             1               5                   10

cag gag cgg ccg gtg agc ctg acc tct acc acc tcc tcg tcg ggc tcc     397
Gln Glu Arg Pro Val Ser Leu Thr Ser Thr Thr Ser Ser Ser Gly Ser
       15                  20                  25

tcc tgt gac agt cgc agt gcc atg gag gag ccc agc agc tcc gag gct     445
Ser Cys Asp Ser Arg Ser Ala Met Glu Glu Pro Ser Ser Ser Glu Ala
     30                  35                  40

ccc gcc aag aat ggg gca ggc tcc ctg aga agc cgg cat ctg ccc aac     493
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Pro Ala Lys Asn Gly Ala Gly Ser Leu Arg Ser Arg His Leu Pro Asn
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agc aac aac aac tcc agc agc tgg ttg aac gtg aag ggg ccc ctc tcc   541
Ser Asn Asn Asn Ser Ser Ser Trp Leu Asn Val Lys Gly Pro Leu Ser
                 65   70   75

ccg ttc aac agc cgg gca gcg gca ggg cct gca cac cac aag ctc agc   589
Pro Phe Asn Ser Arg Ala Ala Ala Gly Pro Ala His His Lys Leu Ser
                 80   85   90

tac ctg ggc cga gtg gtg cgg gag atc gtg gag aca gag cgc atg tac   637
Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu Thr Glu Arg Met Tyr
                 95   100   105

gta cag gac ctg cgc agc atc gtg gag gac tac ctc ttg aag atc att   685
Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr Leu Leu Lys Ile Ile
                 110   115   120

gac aca ccc ggg ctg ctg aag cca gaa cag gtc agc gcc ctc ttt ggg   733
Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val Ser Ala Leu Phe Gly
125   130   135   140

aac ata gaa aac atc tac gcg ctg aac agc cag ctc ctc aga gac ctg   781
Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln Leu Leu Arg Asp Leu
                 145   150   155

gac agc tgc aat agt gac ccc gtg gct gtg gcc agc tgc ttt gtg gaa   829
Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala Ser Cys Phe Val Glu
                 160   165   170

agg agc caa gag ttt gat atc tac act cag tat tgc aac aat tac ccc   877
Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr Cys Asn Asn Tyr Pro
                 175   180   185

aac tcc gtg gcc gcc ctg acg gaa tgc atg cgg gac aag cag cag gcc   925
Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp Lys Gln Gln Ala
                 190   195   200

aag ttc ttt cgg gac cgg cag gag ctg cta cag cac tcg ctg ccc ttg   973
Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His Ser Leu Pro Leu
205   210   215   220

ggc tcc tac ctg ctg aag cca gtc cag cgc atc ctc aag tac cac ctg   1021
Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu Lys Tyr His Leu
          225   230   235

ctg ctc cag gaa att gcc aaa cat ttt gat gaa gaa gag gat ggc ttt   1069
Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu Glu Glu Asp Gly Phe
          240   245   250

gag gtg gtg gag gat gcc att gac acc atg acc tgt gtg gcc tgg tac   1117
Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr Cys Val Ala Trp Tyr
          255   260   265

atc aac gac atg aag agg agg cat gag cac gcg gtc cgg ctc cag gag   1165
Ile Asn Asp Met Lys Arg Arg His Glu His Ala Val Arg Leu Gln Glu
      270   275   280

att cag tca ctc ctc atc aac tgg aag ggg ccc gac ctg acc acc tac   1213
Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro Asp Leu Thr Thr Tyr
285   290   295   300

ggg gag ctt gtc ctg gag ggc aca ttc cgc gtg cat cgc gtg cgc aat   1261
Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val His Arg Val Arg Asn
          305   310   315

gaa agg acc ttt ttc ctc ttt gac aaa aca ctg ctt atc acc aag aag   1309
Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu Leu Ile Thr Lys Lys
          320   325   330

cgg ggc gat cac ttt gtc tac aag ggc aac atc ccg tgc tcc tcc ctg   1357
Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile Pro Cys Ser Ser Leu
          335   340   345

atg ctg atc gaa agc acc aga gac tcc ctg tgc ttc act gtc acc cac   1405

Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys Phe Thr Val Thr His
   350   355   360

tac aag cac agc aag cag cag tac agc atc cag gcc aag aca gtg gag   1453
Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln Ala Lys Thr Val Glu
365   370   375   380

gag aaa cgg aac tgg act cac cac atc aag agg ctc atc cta gag aac   1501
Glu Lys Arg Asn Trp Thr His His Ile Lys Arg Leu Ile Leu Glu Asn
             385   390   395

cac cat gcc acc att ccc cag aag gcc aag gaa gcc atc ttg gaa atg   1549
His His Ala Thr Ile Pro Gln Lys Ala Lys Glu Ala Ile Leu Glu Met
         400   405   410

gat tcc tat tat ccc aat cgg tac cgc tgc agc cca gag cgg ctg aag   1597
Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser Pro Glu Arg Leu Lys
       415   420   425

aag gct tgg tcc tcc cag gat gag gtg tcc acc aat gtg cgc cag ggg   1645
Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr Asn Val Arg Gln Gly
      430   435   440

cgc cgg caa tct gag cca acc aaa cac ctg ctc agg caa ctc aac gag   1693
Arg Arg Gln Ser Glu Pro Thr Lys His Leu Leu Arg Gln Leu Asn Glu
445   450   455   460

aaa gcc cga gca gca gga atg aag cat gca ggc agt gct gga acc ctc   1741
Lys Ala Arg Ala Ala Gly Met Lys His Ala Gly Ser Ala Gly Thr Leu
         465   470   475

ctg gac ttt ggg cag ccc tcc cgt act cgg ggc ctg cag cca gag gct   1789
Leu Asp Phe Gly Gln Pro Ser Arg Thr Arg Gly Leu Gln Pro Glu Ala
         480   485   490

gaa ggg gct acc cag gag gag gaa gag gaa gag gag gag gtg gtg gag   1837
Glu Gly Ala Thr Gln Glu Glu Glu Glu Glu Glu Glu Glu Val Val Glu
   495   500   505

gag gag gag gag gag gag gag gaa gag cag gcc ttt cag gtc tct ctg   1885
Glu Glu Glu Glu Glu Glu Glu Glu Glu Gln Ala Phe Gln Val Ser Leu
    510   515   520

gag gac ctg aca ggg cat gaa ggc aac gag aag ggg gct ggg ccg gag   1933
Glu Asp Leu Thr Gly His Glu Gly Asn Glu Lys Gly Ala Gly Pro Glu
525   530   535   540

ccc cca ggc tca gag gag gag gag gag gag cag gag gag agc ctg gcg   1981
Pro Pro Gly Ser Glu Glu Glu Glu Glu Glu Gln Glu Glu Ser Leu Ala
         545   550   555

gtg gcg gag cag gta gcc gac ttt gcc agc tcc ctg ctg gcc gcc ctc   2029
Val Ala Glu Gln Val Ala Asp Phe Ala Ser Ser Leu Leu Ala Ala Leu
         560   565   570

cac tgc tgg cac tat cgg gcc aac gct tta ctt ttc tcc cgg ggc gct   2077
His Cys Trp His Tyr Arg Ala Asn Ala Leu Leu Phe Ser Arg Gly Ala
         575   580   585

atg gga aag ggg cgc agg gag tct gaa agc tcc agg agc agc aga agg   2125
Met Gly Lys Gly Arg Arg Glu Ser Glu Ser Ser Arg Ser Ser Arg Arg
    590   595   600

ccc agt ggc cgg tct cca acc agt act gag aag cgc atg agc ttc gag   2173
Pro Ser Gly Arg Ser Pro Thr Ser Thr Glu Lys Arg Met Ser Phe Glu
605   610   615   620

tcc att tct tcc ctg cca gag gtt gag ccg gac cct gag gct ggg agt   2221
Ser Ile Ser Ser Leu Pro Glu Val Glu Pro Asp Pro Glu Ala Gly Ser
         625   630   635

gag caa gag gta ttt tct gct gtg gaa ggg ccc agt gcc gag gag acg   2269
Glu Gln Glu Val Phe Ser Ala Val Glu Gly Pro Ser Ala Glu Glu Thr
         640   645   650

cct tca gac aca gaa tct cca gaa gtc ctg gag aca cag ctt gat gcc   2317

Pro Ser Asp Thr Glu Ser Pro Glu Val Leu Glu Thr Gln Leu Asp Ala
      655   660   665

cac cag ggc ctt ctg ggg atg gac ccc cca ggt gac atg gtg gac ttc   2365
His Gln Gly Leu Leu Gly Met Asp Pro Pro Gly Asp Met Val Asp Phe
    670   675   680

gtg gca gct gag agc act gag gac ctt aag gcc ctg agc agc gag gag   2413
Val Ala Ala Glu Ser Thr Glu Asp Leu Lys Ala Leu Ser Ser Glu Glu
685   690   695   700

gaa gaa gaa atg gga ggt gcc gcc cag gag cct gag agc ctt ctg cca   2461
Glu Glu Glu Met Gly Gly Ala Ala Gln Glu Pro Glu Ser Leu Leu Pro
      705   710   715

ccc tcc gtg ctg gac cag gcc agc gtc att gcg gag cga ttt gtc agc   2509
Pro Ser Val Leu Asp Gln Ala Ser Val Ile Ala Glu Arg Phe Val Ser
      720   725   730

agc ttc tct cgg cgg agc agc gtg gca cag gag gac agc aag tcc agt   2557
Ser Phe Ser Arg Arg Ser Ser Val Ala Gln Glu Asp Ser Lys Ser Ser
      735   740   745

ggc ttt ggg agc ccg cgg ctg gtc agc cgg agc agc agc gtg ctc agc   2605
Gly Phe Gly Ser Pro Arg Leu Val Ser Arg Ser Ser Ser Val Leu Ser
    750   755   760

ctg gag ggc agc gag aag ggc ctg gcc cgg cat ggc agt gcc aca gac   2653
Leu Glu Gly Ser Glu Lys Gly Leu Ala Arg His Gly Ser Ala Thr Asp
765   770   775   780

tcc ctc agc tgt cag ctc tcc cca gaa gtg gac atc agt gtg ggg gtg   2701
Ser Leu Ser Cys Gln Leu Ser Pro Glu Val Asp Ile Ser Val Gly Val
        785   790   795

gcc aca gag gac agc cct tct gtc aat ggg atg gag ccc cca agc cca   2749
Ala Thr Glu Asp Ser Pro Ser Val Asn Gly Met Glu Pro Pro Ser Pro
     800   805   810

ggc tgc cca gtg gag cct gac cgg tct tcc tgc aag aag aag gaa tca   2797
Gly Cys Pro Val Glu Pro Asp Arg Ser Ser Cys Lys Lys Lys Glu Ser
          815   820   825

gca ctc tcc acc cga gac cgg ctg ttg cta gac aag att aag agc tat   2845
Ala Leu Ser Thr Arg Asp Arg Leu Leu Leu Asp Lys Ile Lys Ser Tyr
          830   835   840

tat gaa aat gca gaa cac cat gat gca ggc ttc agc gtc cgt cgc cgg   2893
Tyr Glu Asn Ala Glu His His Asp Ala Gly Phe Ser Val Arg Arg Arg
845   850   855   860

gag agc ctc tcc tac atc ccc aaa gga ctg gta aga aac tcc atc tcc   2941
Glu Ser Leu Ser Tyr Ile Pro Lys Gly Leu Val Arg Asn Ser Ile Ser
                   865   870   875

agg ttc aac agc ctt ccc cgg cca gac cca gag cca gta cct cca gtg   2989
Arg Phe Asn Ser Leu Pro Arg Pro Asp Pro Glu Pro Val Pro Pro Val
                   880   885   890

ggg agc aag aga cag gtg ggc tcc cgg ccg act tcg tgg gcc ctg ttt   3037
Gly Ser Lys Arg Gln Val Gly Ser Arg Pro Thr Ser Trp Ala Leu Phe
          895   900   905

gag ctc cca gga cca agc cag gca gtc aaa ggg gac cca cct ccc atc   3085
Glu Leu Pro Gly Pro Ser Gln Ala Val Lys Gly Asp Pro Pro Pro Ile
          910   915   920

tca gat gct gag ttc cgc cca tct tca gaa att gtg aag atc tgg gag   3133
Ser Asp Ala Glu Phe Arg Pro Ser Ser Glu Ile Val Lys Ile Trp Glu
925   930   935   940

gga atg gag tct tcc gga ggg agc cct ggg aag ggg cca ggc cag ggc   3181
Gly Met Glu Ser Ser Gly Gly Ser Pro Gly Lys Gly Pro Gly Gln Gly
                   945   950   955

cag gcc aat ggc ttt gac ctg cat gag cca ctc ttc atc ctg gag gag   3229

Gln Ala Asn Gly Phe Asp Leu His Glu Pro Leu Phe Ile Leu Glu Glu
            960   965   970

cat gag ctg gga gcc atc aca gag gag tcg gcc act gcc tcc ccg gaa   3277
His Glu Leu Gly Ala Ile Thr Glu Glu Ser Ala Thr Ala Ser Pro Glu
         975   980   985

agc tcc tct ccc act gag ggg cgc agc ccg gcc cac ctg gcc cgg gag   3325
Ser Ser Ser Pro Thr Glu Gly Arg Ser Pro Ala His Leu Ala Arg Glu
          990   995   1000

ctg aaa gag ctg gtg aag gag ctg agc agc agt acc cag ggg gag   3370
Leu Lys Glu Leu Val Lys Glu Leu Ser Ser Ser Thr Gln Gly Glu
1005   1010   1015

ctg gtg gcc cca ctg cac ccc cgc atc gtg cag ctc tcc cac gta   3415
Leu Val Ala Pro Leu His Pro Arg Ile Val Gln Leu Ser His Val
1020   1025   1030

atg gac agc cac gtg agc gag cgc gtc aag aac aag gtc tac cag   3460
Met Asp Ser His Val Ser Glu Arg Val Lys Asn Lys Val Tyr Gln
1035   1040   1045

ctg gcc cgc cag tac agc ctc cgg atc aag agc aac aag cca gtg   3505
Leu Ala Arg Gln Tyr Ser Leu Arg Ile Lys Ser Asn Lys Pro Val
1050   1055   1060

atg gcc agg cca cca ctg cag tgg gaa aag gtg gcc cct gag agg   3550
Met Ala Arg Pro Pro Leu Gln Trp Glu Lys Val Ala Pro Glu Arg
1065   1070   1075

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Asp Gly Lys Ser Pro Thr Val Pro Cys Leu Gln Glu Glu Ala Gly
1080   1085   1090

gag cca tta ggt ggc aaa ggt aag agg aag ccg gtg ctg tct cta   3640
Glu Pro Leu Gly Gly Lys Gly Lys Arg Lys Pro Val Leu Ser Leu
1095   1100   1105

ttt gac tat gag cag ctg atg gcc cag gag cac agc cct ccc aag   3685
Phe Asp Tyr Glu Gln Leu Met Ala Gln Glu His Ser Pro Pro Lys
1110   1115   1120

ccc tcc tcg gct ggg gag atg tca cca cag cgt ttc ttc ttc aac   3730
Pro Ser Ser Ala Gly Glu Met Ser Pro Gln Arg Phe Phe Phe Asn
1125   1130   1135

ccg tct gct gtc agc cag agg acc acc tcg cct ggg ggc cgg ccc   3775
Pro Ser Ala Val Ser Gln Arg Thr Thr Ser Pro Gly Gly Arg Pro
1140   1145   1150

tcc gcc tgg agc ccc ctc agc ccc aca gag acc ttc agc tgg ccc   3820
Ser Ala Trp Ser Pro Leu Ser Pro Thr Glu Thr Phe Ser Trp Pro
1155   1160   1165

gac gtc cgt gag ctc tgc tcc aag tat gcc tcc cgc gat gag gca   3865
Asp Val Arg Glu Leu Cys Ser Lys Tyr Ala Ser Arg Asp Glu Ala
1170   1175   1180

cgc cga gca ggg ggc ggc cgg ccc cgc ggc cca ccc gtc aac agg   3910
Arg Arg Ala Gly Gly Gly Arg Pro Arg Gly Pro Pro Val Asn Arg
1185   1190   1195

agc cac tcg gtg ccg gag aac atg gta gag cca cct ctg tcg ggc   3955
Ser His Ser Val Pro Glu Asn Met Val Glu Pro Pro Leu Ser Gly
1200   1205   1210

agg gtg ggc cgc tgc cgc agc ctg agc acc aag agg ggc cgg gga   4000
Arg Val Gly Arg Cys Arg Ser Leu Ser Thr Lys Arg Gly Arg Gly
1215   1220   1225

ggc gga gag gct gcc caa tcc cct ggg cct ctg ccc cag agc aag   4045
Gly Gly Glu Ala Ala Gln Ser Pro Gly Pro Leu Pro Gln Ser Lys
1230   1235   1240

ccg gat gga ggc gag acc ctg tat gtc act gca gac ctc acc ctg   4090

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Pro  Asp Gly Gly Glu Thr  Leu Tyr Val Thr Ala  Asp Leu Thr Leu
1245             1250                1255


gag  gac aac cgg cgg gtg · att gtc atg gag aag  gga ccc ctt ccc     4135
Glu  Asp Asn Arg Arg Val  Ile Val Met Glu Lys  Gly Pro Leu Pro
1260             1265                1270


agc  ccc act gca ggg ctg  gag gag agc agt ggc  cag gga cca agc     4180
Ser  Pro Thr Ala Gly Leu  Glu Glu Ser Ser Gly  Gln Gly Pro Ser
1275             1280                1285


tca  ccg gtg gcc ctg ctg  ggg cag gtt cag gac  ttc cag cag tct     4225
Ser  Pro Val Ala Leu Leu  Gly Gln Val Gln Asp  Phe Gln Gln Ser
1290             1295                1300


gca  gag tgc cag ccg aag  gaa gag ggt tcc agg  gac ccg gca gac     4270
Ala  Glu Cys Gln Pro Lys  Glu Glu Gly Ser Arg  Asp Pro Ala Asp
1305             1310                1315


ccg  agc cag cag ggc aga  gtg aga aac ctt aga  gag aag ttc cag     4315
Pro  Ser Gln Gln Gly Arg  Val Arg Asn Leu Arg  Glu Lys Phe Gln
1320             1325                1330


gcc  ttg aac tct gtc ggt  tga tgctgactcc tgggggaggg aggagtcatg     4366
Ala  Leu Asn Ser Val Gly
1335             1340


ttggaggttg gggaagaacc tgggcatcct tcccctcaag cctgggctca tggagcccct   4426


gcccagggcc ctcaggtggg cggaaagtcc atcccctccg cccttcagga aggatgctcc   4486


cgtgtgcagg ggtctcctgc ctgtgccatc cactggggct cgagacaatt tcccactcac   4546


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atttaagctc acttcttccc agagagagga agctctgctc aggcctccag cgttggctgg   4666


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            35   40   45

Gly Ala Gly Ser Leu Arg Ser Arg His Leu Pro Asn Ser Asn Asn Asn
        50   55   60

Ser Ser Ser Trp Leu Asn Val Lys Gly Pro Leu Ser Pro Phe Asn Ser
65   70   75   80

Arg Ala Ala Ala Gly Pro Ala His His Lys Leu Ser Tyr Leu Gly Arg
                85   90   95

Val Val Arg Glu Ile Val Glu Thr Glu Arg Met Tyr Val Gln Asp Leu
                100   105   110

Arg Ser Ile Val Glu Asp Tyr Leu Leu Lys Ile Ile Asp Thr Pro Gly
                115   120   125

Leu Leu Lys Pro Glu Gln Val Ser Ala Leu Phe Gly Asn Ile Glu Asn
            130   135   140

Ile Tyr Ala Leu Asn Ser Gln Leu Leu Arg Asp Leu Asp Ser Cys Asn
145   150   155   160

Ser Asp Pro Val Ala Val Ala Ser Cys Phe Val Glu Arg Ser Gln Glu
                165   170   175

Phe Asp Ile Tyr Thr Gln Tyr Cys Asn Asn Tyr Pro Asn Ser Val Ala
                180   185   190

Ala Leu Thr Glu Cys Met Arg Asp Lys Gln Gln Ala Lys Phe Phe Arg
                195   200   205

Asp Arg Gln Glu Leu Leu Gln His Ser Leu Pro Leu Gly Ser Tyr Leu
            210   215   220

Leu Lys Pro Val Gln Arg Ile Leu Lys Tyr His Leu Leu Leu Gln Glu

225   230   235   240

Ile Ala Lys His Phe Asp Glu Glu Glu Asp Gly Phe Glu Val Val Glu
             245   250   255

Asp Ala Ile Asp Thr Met Thr Cys Val Ala Trp Tyr Ile Asn Asp Met
             260   265   270

Lys Arg Arg His Glu His Ala Val Arg Leu Gln Glu Ile Gln Ser Leu
          275   280   285

Leu Ile Asn Trp Lys Gly Pro Asp Leu Thr Thr Tyr Gly Glu Leu Val
      290   295   300

Leu Glu Gly Thr Phe Arg Val His Arg Val Arg Asn Glu Arg Thr Phe
305   310   315   320

Phe Leu Phe Asp Lys Thr Leu Leu Ile Thr Lys Lys Arg Gly Asp His
             325   330   335

Phe Val Tyr Lys Gly Asn Ile Pro Cys Ser Ser Leu Met Leu Ile Glu
             340   345   350

Ser Thr Arg Asp Ser Leu Cys Phe Thr Val Thr His Tyr Lys His Ser
          355   360   365

Lys Gln Gln Tyr Ser Ile Gln Ala Lys Thr Val Glu Glu Lys Arg Asn
      370   375   380

Trp Thr His His Ile Lys Arg Leu Ile Leu Glu Asn His His Ala Thr
385   390   395   400

Ile Pro Gln Lys Ala Lys Glu Ala Ile Leu Glu Met Asp Ser Tyr Tyr
               405   410   415

Pro Asn Arg Tyr Arg Cys Ser Pro Glu Arg Leu Lys Lys Ala Trp Ser
               420   425   430

Ser Gln Asp Glu Val Ser Thr Asn Val Arg Gln Gly Arg Arg Gln Ser
          435   440   445

Glu Pro Thr Lys His Leu Leu Arg Gln Leu Asn Glu Lys Ala Arg Ala
     450   455   460

Ala Gly Met Lys His Ala Gly Ser Ala Gly Thr Leu Leu Asp Phe Gly
465   470   475   480

Gln Pro Ser Arg Thr Arg Gly Leu Gln Pro Glu Ala Glu Gly Ala Thr
               485   490   495

Gln Glu Glu Glu Glu Glu Glu Glu Glu Val Val Glu Glu Glu Glu Glu
          500   505   510

Glu Glu Glu Glu Glu Gln Ala Phe Gln Val Ser Leu Glu Asp Leu Thr
     515   520   525

Gly His Glu Gly Asn Glu Lys Gly Ala Gly Pro Glu Pro Pro Gly Ser

530   535   540

Glu Glu Glu Glu Glu Glu Gln Glu Glu Ser Leu Ala Val Ala Glu Gln
545   550   555   560

Val Ala Asp Phe Ala Ser Ser Leu Leu Ala Ala Leu His Cys Trp His
                565   570   575

Tyr Arg Ala Asn Ala Leu Leu Phe Ser Arg Gly Ala Met Gly Lys Gly
                580   585   590

Arg Arg Glu Ser Glu Ser Ser Arg Ser Ser Arg Arg Pro Ser Gly Arg
                595   600   605

Ser Pro Thr Ser Thr Glu Lys Arg Met Ser Phe Glu Ser Ile Ser Ser
                610   615   620

Leu Pro Glu Val Glu Pro Asp Pro Glu Ala Gly Ser Glu Gln Glu Val
625   630   635   640

Phe Ser Ala Val Glu Gly Pro Ser Ala Glu Glu Thr Pro Ser Asp Thr
                645   650   655

Glu Ser Pro Glu Val Leu Glu Thr Gln Leu Asp Ala His Gln Gly Leu
                660   665   670

Leu Gly Met Asp Pro Pro Gly Asp Met Val Asp Phe Val Ala Ala Glu
                675   680   685

Ser Thr Glu Asp Leu Lys Ala Leu Ser Ser Glu Glu Glu Glu Met
   690   695   700

Gly Gly Ala Ala Gln Glu Pro Glu Ser Leu Leu Pro Pro Ser Val Leu
705   710   715   .   720

Asp Gln Ala Ser Val Ile Ala Glu Arg Phe Val Ser Ser Phe Ser Arg
        725   730   735

Arg Ser Ser Val Ala Gln Glu Asp Ser Lys Ser Ser Gly Phe Gly Ser
       740   745   750

Pro Arg Leu Val Ser Arg Ser Ser Ser Val Leu Ser Leu Glu Gly Ser
      755   760   765

Glu Lys Gly Leu Ala Arg His Gly Ser Ala Thr Asp Ser Leu Ser Cys
   770   775   780

Gln Leu Ser Pro Glu Val Asp Ile Ser Val Gly Val Ala Thr Glu Asp
785   790   795   800

Ser Pro Ser Val Asn Gly Met Glu Pro Pro Ser Pro Gly Cys Pro Val
        805   810   815

Glu Pro Asp Arg Ser Ser Cys Lys Lys Lys Glu Ser Ala Leu Ser Thr
      820   825   830

Arg Asp Arg Leu Leu Leu Asp Lys Ile Lys Ser Tyr Tyr Glu Asn Ala

835   840   845

Glu His His Asp Ala Gly Phe Ser Val Arg Arg Arg Glu Ser Leu Ser
   850   855   860

Tyr Ile Pro Lys Gly Leu Val Arg Asn Ser Ile Ser Arg Phe Asn Ser
865   870   875   880

Leu Pro Arg Pro Asp Pro Glu Pro Val Pro Pro Val Gly Ser Lys Arg
       885   890   895

Gln Val Gly Ser Arg Pro Thr Ser Trp Ala Leu Phe Glu Leu Pro Gly
     900   905   910

Pro Ser Gln Ala Val Lys Gly Asp Pro Pro Pro Ile Ser Asp Ala Glu
     915   920   925

Phe Arg Pro Ser Ser Glu Ile Val Lys Ile Trp Glu Gly Met Glu Ser
   930   935   940

Ser Gly Gly Ser Pro Gly Lys Gly Pro Gly Gln Gly Gln Ala Asn Gly
945   950   955   960

Phe Asp Leu His Glu Pro Leu Phe Ile Leu Glu Glu His Glu Leu Gly
       965   970   975

Ala Ile Thr Glu Glu Ser Ala Thr Ala Ser Pro Glu Ser Ser Ser Pro
       980   985   990

Thr Glu Gly Arg Ser Pro Ala His Leu Ala Arg Glu Leu Lys Glu Leu
    995   1000   1005

Val Lys Glu Leu Ser Ser Ser Thr Gln Gly Glu Leu Val Ala Pro
   1010   1015   1020

Leu His Pro Arg Ile Val Gln Leu Ser His Val Met Asp Ser His
   1025   1030   1035

Val Ser Glu Arg Val Lys Asn Lys Val Tyr Gln Leu Ala Arg Gln
   1040   1045   1050

Tyr Ser Leu Arg Ile Lys Ser Asn Lys Pro Val Met Ala Arg Pro
   1055   1060   1065

Pro Leu Gln Trp Glu Lys Val Ala Pro Glu Arg Asp Gly Lys Ser
   1070   1075   1080

Pro Thr Val Pro Cys Leu Gln Glu Glu Ala Gly Glu Pro Leu Gly
   1085   1090   1095

Gly Lys Gly Lys Arg Lys Pro Val Leu Ser Leu Phe Asp Tyr Glu
   1100   1105   1110

Gln Leu Met Ala Gln Glu His Ser Pro Pro Lys Pro Ser Ser Ala
   1115   1120   1125

Gly Glu Met Ser Pro Gln Arg Phe Phe Phe Asn Pro Ser Ala Val

1130   1135   1140

Ser Gln Arg Thr Thr Ser Pro Gly Gly Arg Pro Ser Ala Trp Ser
   1145   1150   1155

Pro Leu Ser Pro Thr Glu Thr Phe Ser Trp Pro Asp Val Arg Glu
   1160   1165   1170

Leu Cys Ser Lys Tyr Ala Ser Arg Asp Glu Ala Arg Arg Ala Gly
   1175   1180   1185

Gly Gly Arg Pro Arg Gly Pro Pro Val Asn Arg Ser His Ser Val
   1190   1195   1200

Pro Glu Asn Met Val Glu Pro Pro Leu Ser Gly Arg Val Gly Arg
   1205   1210   1215

Cys Arg Ser Leu Ser Thr Lys Arg Gly Arg Gly Gly Gly Glu Ala
   1220   1225   1230

Ala Gln Ser Pro Gly Pro Leu Pro Gln Ser Lys Pro Asp Gly Gly
   1235   1240   1245

Glu Thr Leu Tyr Val Thr Ala Asp Leu Thr Leu Glu Asp Asn Arg
   1250   1255   1260

Arg Val Ile Val Met Glu Lys Gly Pro Leu Pro Ser Pro Thr Ala
   1265   1270   1275

Gly Leu Glu Glu Ser Ser Gly Gln Gly Pro Ser Ser Pro Val Ala
     1280   1285   1290

Leu Leu Gly Gln Val Gln Asp Phe Gln Gln Ser Ala Glu Cys Gln
     1295   1300   1305

Pro Lys Glu Glu Gly Ser Arg Asp Pro Ala Asp Pro Ser Gln Gln
     1310   1315   1320

Gly Arg Val Arg Asn Leu Arg Glu Lys Phe Gln Ala Leu Asn Ser
     1325   1330   1335

Val Gly
     1340

<210> 3
<211> 1095
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A partial sequence of SEQ ID NO:1 consisting of the 581st to the
      1675th nucleotides that comprises a region encoding Dbl homology
      domain and Pleckstrin homology domain, which encodes the amino ac
      id sequence of SEQ ID NO:4.

<220>
<221> CDS
<222> (1)..(1095)

<400> 3

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aag ctc agc tac ctg ggc cga gtg gtg cgg gag atc gtg gag aca gag        48
Lys Leu Ser Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu Thr Glu
1               5                   10                  15


cgc atg tac gta cag gac ctg cgc agc atc gtg gag gac tac ctc ttg        96
Arg Met Tyr Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr Leu Leu
                20                  25                  30


aag atc att gac aca ccc ggg ctg ctg aag cca gaa cag gtc agc gcc        144
Lys Ile Ile Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val Ser Ala
        35                  40                  45


ctc ttt ggg aac ata gaa aac atc tac gcg ctg aac agc cag ctc ctc        192
Leu Phe Gly Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln Leu Leu
        50                  55                  60


aga gac ctg gac agc tgc aat agt gac ccc gtg gct gtg gcc agc tgc        240
Arg Asp Leu Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala Ser Cys
65              70                  75                  80


ttt gtg gaa agg agc caa gag ttt gat atc tac act cag tat tgc aac        288
Phe Val Glu Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr Cys Asn
                85                  90                  95


aat tac ccc aac tcc gtg gcc gcc ctg acg gaa tgc atg cgg gac aag        336
Asn Tyr Pro Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp Lys
                100                 105                 110


cag cag gcc aag ttc ttt cgg gac cgg cag gag ctg cta cag cac tcg        384
Gln Gln Ala Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His Ser
        115                 120                 125


ctg ccc ttg ggc tcc tac ctg ctg aag cca gtc cag cgc atc ctc aag        432
Leu Pro Leu Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu Lys
        130                 135                 140


tac cac ctg ctg ctc cag gaa att gcc aaa cat ttt gat gaa gaa gag        480
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Tyr His Leu Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu Glu Glu
145   150   155   160

gat ggc ttt gag gtg gtg gag gat gcc att gac acc atg acc tgt gtg   528
Asp Gly Phe Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr Cys Val
            165   170   175

gcc tgg tac atc aac gac atg aag agg agg cat gag cac gcg gtc cgg   576
Ala Trp Tyr Ile Asn Asp Met Lys Arg Arg His Glu His Ala Val Arg
            180   185   190

ctc cag gag att cag tca ctc ctc atc aac tgg aag ggg ccc gac ctg   624
Leu Gln Glu Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro Asp Leu
            195   200   205

acc acc tac ggg gag ctt gtc ctg gag ggc aca ttc cgc gtg cat cgc   672
Thr Thr Tyr Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val His Arg
        210   215   220

gtg cgc aat gaa agg acc ttt ttc ctc ttt gac aaa aca ctg ctt atc   720
Val Arg Asn Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu Leu Ile
225   230   235   240

acc aag aag cgg ggc gat cac ttt gtc tac aag ggc aac atc ccg tgc   768
Thr Lys Lys Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile Pro Cys
            245   250   255

tcc tcc ctg atg ctg atc gaa agc acc aga gac tcc ctg tgc ttc act   816
Ser Ser Leu Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys Phe Thr
            260   265   270

gtc acc cac tac aag cac agc aag cag cag tac agc atc cag gcc aag   864
Val Thr His Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln Ala Lys
            275   280   285

aca gtg gag gag aaa cgg aac tgg act cac cac atc aag agg ctc atc   912
Thr Val Glu Glu Lys Arg Asn Trp Thr His His Ile Lys Arg Leu Ile
            290   295   300

cta gag aac cac cat gcc acc att ccc cag aag gcc aag gaa gcc atc   960
Leu Glu Asn His His Ala Thr Ile Pro Gln Lys Ala Lys Glu Ala Ile
305   310   315   320

ttg gaa atg gat tcc tat tat ccc aat cgg tac cgc tgc agc cca gag   1008
Leu Glu Met Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser Pro Glu
                 325   330   335

cgg ctg aag aag gct tgg tcc tcc cag gat gag gtg tcc acc aat gtg   1056
Arg Leu Lys Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr Asn Val
                 340   345   350

cgc cag ggg cgc cgg caa tct gag cca acc aaa cac ctg   1095
Arg Gln Gly Arg Arg Gln Ser Glu Pro Thr Lys His Leu
                 355   360   365

<210> 4
<211> 365
<212> PRT
<213> Homo sapiens

<400> 4

Lys Leu Ser Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu Thr Glu
1   5   10   15

Arg Met Tyr Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr Leu Leu
                 20   25   30

Lys Ile Ile Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val Ser Ala
                 35   40   45

Leu Phe Gly Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln Leu Leu

50 · 55 60

Arg Asp Leu Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala Ser Cys
65 70 75 80

Phe Val Glu Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr Cys Asn
85 90 95

Asn Tyr Pro Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp Lys
100 105 110

Gln Gln Ala Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His Ser
115 120 125

Leu Pro Leu Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu Lys
130 135 140

Tyr His Leu Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu Glu Glu
145 150 155 160

Asp Gly Phe Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr Cys Val
165 170 175

Ala Trp Tyr Ile Asn Asp Met Lys Arg Arg His Glu His Ala Val Arg
180 185 190

Leu Gln Glu Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro Asp Leu
195 200 205

Thr Thr Tyr Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val His Arg
          210   215   220

Val Arg Asn Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu Leu Ile
225   230   235   240

Thr Lys Lys Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile Pro Cys
                245   250   255

Ser Ser Leu Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys Phe Thr
          260   265   270

Val Thr His Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln Ala Lys
          275   280   285

Thr Val Glu Glu Lys Arg Asn Trp Thr His His Ile Lys Arg Leu Ile
          290   295   300

Leu Glu Asn His His Ala Thr Ile Pro Gln Lys Ala Lys Glu Ala Ile
305   310   315   320

Leu Glu Met Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser Pro Glu
                325   330   335

Arg Leu Lys Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr Asn Val
                340   345   350

Arg Gln Gly Arg Arg Gln Ser Glu Pro Thr Lys His Leu

355   360   365

<210> 5
<211> 1102
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Polynucleotide having kozak consensus sequence and
      methionine codon in its 5'-terminal, followed by partial sequen
      ce of SEQ ID NO:1 of the 581st to 1675th nucleotides having
      a region encoding Dbl homology domain and Pleckstri
      n homology domain, encoding SEQ ID NO:6.

<220>
<221> CDS
<222> (5)..(1102)

<220>
<221> misc_feature
<222> (1)..(4)
<223> kozak consensus sequence

<220>
<221> misc_feature
<222> (5)..(7)
<223> methionine codon

<400> 5
cacc atg aag ctc agc tac ctg ggc cga gtg gtg cgg gag atc gtg gag   49
     Met Lys Leu Ser Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu
    1   5   10   15

aca gag cgc atg tac gta cag gac ctg cgc agc atc gtg gag gac tac   97
Thr Glu Arg Met Tyr Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr
                20   25   30

ctc ttg aag atc att gac aca ccc ggg ctg ctg aag cca gaa cag gtc   145
Leu Leu Lys Ile Ile Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val
              35   40   45

agc gcc ctc ttt ggg aac ata gaa aac atc tac gcg ctg aac agc cag   193
Ser Ala Leu Phe Gly Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln
          50   55   60

ctc ctc aga gac ctg gac agc tgc aat agt gac ccc gtg gct gtg gcc   241
Leu Leu Arg Asp Leu Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala
        65   70   75

agc tgc ttt gtg gaa agg agc caa gag ttt gat atc tac act cag tat   289
Ser Cys Phe Val Glu Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr
80   85   90   95

tgc aac aat tac ccc aac tcc gtg gcc gcc ctg acg gaa tgc atg cgg   337
Cys Asn Asn Tyr Pro Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg
                100   105   110

gac aag cag cag gcc aag ttc ttt cgg gac cgg cag gag ctg cta cag   385
Asp Lys Gln Gln Ala Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln
              115   120   125

cac tcg ctg ccc ttg ggc tcc tac ctg ctg aag cca gtc cag cgc atc   433
His Ser Leu Pro Leu Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile
          130   135   140

ctc aag tac cac ctg ctg ctc cag gaa att gcc aaa cat ttt gat gaa   481
Leu Lys Tyr His Leu Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu
       145   150   155

gaa gag gat ggc ttt gag gtg gtg gag gat gcc att gac acc atg acc   529

Glu Glu Asp Gly Phe Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr
160   165   170   175

tgt gtg gcc tgg tac atc aac gac atg aag agg agg cat gag cac gcg   577
Cys Val Ala Trp Tyr Ile Asn Asp Met Lys Arg Arg His Glu His Ala
                    180   185   190

gtc cgg ctc cag gag att cag tca ctc ctc atc aac tgg aag ggg ccc   625
Val Arg Leu Gln Glu Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro
                195   200   205

gac ctg acc acc tac ggg gag ctt gtc ctg gag ggc aca ttc cgc gtg   673
Asp Leu Thr Thr Tyr Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val
            210   215   220

cat cgc gtg cgc aat gaa agg acc ttt ttc ctc ttt gac aaa aca ctg   721
His Arg Val Arg Asn Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu
        225   230   235

ctt atc acc aag aag cgg ggc gat cac ttt gtc tac aag ggc aac atc   769
Leu Ile Thr Lys Lys Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile
240   245   250   255

ccg tgc tcc tcc ctg atg ctg atc gaa agc acc aga gac tcc ctg tgc   817
Pro Cys Ser Ser Leu Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys
                    260   265   270

ttc act gtc acc cac tac aag cac agc aag cag cag tac agc atc cag   865
Phe Thr Val Thr His Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln
                275   280   285

gcc aag aca gtg gag gag aaa cgg aac tgg act cac cac atc aag agg   913
Ala Lys Thr Val Glu Glu Lys Arg Asn Trp Thr His His Ile Lys Arg
            290   295   300

ctc atc cta gag aac cac cat gcc acc att ccc cag aag gcc aag gaa   961
Leu Ile Leu Glu Asn His His Ala Thr Ile Pro Gln Lys Ala Lys Glu
        305   310   315

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gcc atc ttg gaa atg gat tcc tat tat ccc aat cgg tac cgc tgc agc      1009
Ala Ile Leu Glu Met Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser
320              325              330              335


cca gag cgg ctg aag aag gct tgg tcc tcc cag gat gag gtg tcc acc      1057
Pro Glu Arg Leu Lys Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr
                340              345              350


aat gtg cgc cag ggg cgc cgg caa tct gag cca acc aaa cac ctg          1102
Asn Val Arg Gln Gly Arg Arg Gln Ser Glu Pro Thr Lys His Leu
                355              360              365
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<210> 6
<211> 366
<212> PRT
<213> Homo sapiens

<400> 6

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Met Lys Leu Ser Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu Thr
1               5                10               15


Glu Arg Met Tyr Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr Leu
                20               25               30


Leu Lys Ile Ile Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val Ser
        35               40               45


Ala Leu Phe Gly Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln Leu
     50               55               60     .


Leu Arg Asp Leu Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala Ser
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65   70   75   80

Cys Phe Val Glu Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr Cys
          85   90   95

Asn Asn Tyr Pro Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp
       100   105   110

Lys Gln Gln Ala Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His
     115   120   125

Ser Leu Pro Leu Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu
   130   135   140

Lys Tyr His Leu Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu Glu
145   150   155   160

Glu Asp Gly Phe Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr Cys
         165   170   175

Val Ala Trp Tyr Ile Asn Asp Met Lys Arg Arg His Glu His Ala Val
       180   185   190

Arg Leu Gln Glu Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro Asp
     195   200   205

Leu Thr Thr Tyr Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val His
     210   215   220

Arg Val Arg Asn Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu Leu
225   230   235   240

Ile Thr Lys Lys Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile Pro
              245   250   255

Cys Ser Ser Leu Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys Phe
              260   265   270

Thr Val Thr His Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln Ala
           275   280   285

Lys Thr Val Glu Glu Lys Arg Asn Trp Thr His His Ile Lys Arg Leu
        290   295   300

Ile Leu Glu Asn His His Ala Thr Ile Pro Gln Lys Ala Lys Glu Ala
305   310   315   320

Ile Leu Glu Met Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser Pro
              325   330   335

Glu Arg Leu Lys Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr Asn
              340   345   350

Val Arg Gln Gly Arg Arg Gln Ser Glu Pro Thr Lys His Leu
           355   360   365

<210> 7

<211> 22
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of SEQ ID NO:1 for
use as a primer

<400> 7
gggagatgtc accacagcgt tt   22

<210> 8
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of SEQ ID NO:1 for
use as a primer

<400> 8
aatggatccc gaccgacaga gttcaaggc   29

<210> 9
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of SEQ ID NO:1 for
use as a primer

<400> 9
caccatgaag ctcagctacc tgggccgagt ggtg   34

<210> 10
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of SEQ ID NO:1 for
use as a primer

<400> 10
caggtgtttg gttggctcag attgcc   26

<210> 11
<211> 35
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of proto-Dbl for us
e as a primer

<400> 11
aatagatctg gaaatggcag ttttaaagaa ccacg   35

<210> 12
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of proto-Dbl for us
e as a primer

<400> 12
aatgtcgacc tgcttcaaca aaatatttc   29

<210> 13
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of Cdc42 for use as
a primer

<400> 13
caccatgcag acaattaagt gtgttgttg   29

<210> 14
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of Cdc42 for use as
a primer

<400> 14
tcatagcagc acacacctgc ggctc   25

<210> 15
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of RhoA for use as
a primer

<400> 15
caccatggct gccatccgga agaaactgg   29

<210> 16
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of RhoA for use as
a primer

<400> 16
tcacaagaca aggcaaccag attttttc   28

<210> 17
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of Rac1 for use as
a primer

<400> 17
caccatgcag gccatcaagt gtgtggtgg   29

<210> 18
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Designed polynucleotide based on the sequence of Rac1 for use as
a primer

<400> 18

ttacaacagc aggcattttc tcttcc   26

<210> 19
<211> 7
<212> DNA
<213> artificial

<220>
<223> Designed oligonucleotide including Kozak consensus sequence follo
      wed by a methionine codon.

<400> 19
caccatg   7

<210> 20
<211> 576
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<223> Cdc42 gene

<400> 20
atgcagacaa ttaagtgtgt tgttgtgggc gatggtgctg ttggtaaaac atgtctcctg   60

atatcctaca caacaaacaa atttccatcg gaatatgtac cgactgtttt tgacaactat   120

gcagtcacag ttatgattgg tggagaacca tatactcttg gactttttga tactgcaggg   180

caagaggatt atgacagatt acgaccgctg agttatccac aaacagatgt atttctagtc   240

tgttttttcag tggtctctcc atcttcattt gaaaacgtga aagaaaagtg ggtgcctgag   300

ataactcacc actgtccaaa gactcctttc ttgcttgttg ggactcaaat tgatctcaga   360

gatgacccct ctactattga gaaacttgcc aagaacaaac agaagcctat cactccagag   420

actgctgaaa agctggcccg tgacctgaag gctgtcaagt atgtggagtg ttctgcactt   480

acacagaaag gcctaaagaa tgtatttgac gaagcaatat tggctgccct ggagcctcca   540

gaaccgaaga agagccgcag gtgtgtgctg ctatga   576

<210> 21
<211> 191
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Cdc42

<400> 21

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys
1   5   10   15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser Glu Tyr
            20   25   30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile Gly Gly
            35   40   45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr
        50   55   60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Val
65   70   75   80

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys Glu Lys
                85   90   95

Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe Leu Leu
                100   105   110

Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr Ile Glu Lys
            115   120   125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr Ala Glu Lys
        130   135   140

Leu Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys Ser Ala Leu
145   150   155   160

Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu Ala Ala
                165   170   175

Leu Glu Pro Pro Glu Pro Lys Lys Ser Arg Arg Cys Val Leu Leu
                180   185   190

<210> 22
<211> 582
<212> DNA
<213> homo sapiens

<220>

<221> misc_feature
<223> RhoA gene

<400> 22
atggctgcca tccggaagaa actggtgatt gttggtgatg gagcctgtgg aaagacatgc   60

ttgctcatag tcttcagcaa ggaccagttc ccagaggtgt atgtgcccac agtgtttgag   120

aactatgtgg cagatatcga ggtggatgga aagcaggtag agttggcttt gtgggacaca   180

gctgggcagg aagattatga tcgcctgagg cccctctcct acccagatac cgatgttata   240

ctgatgtgtt tttccatcga cagccctgat agtttagaaa acatcccaga aaagtggacc   300

ccagaagtca agcatttctg tcccaacgtg cccatcatcc tggttgggaa taagaaggat   360

cttcggaatg atgagcacac aaggcgggag ctagccaaga tgaagcagga gccggtgaaa   420

cctgaagaag gcagagatat ggcaaacagg attggcgctt ttgggtacat ggagtgttca   480

gcaaagacca aagatggagt gagagaggtt tttgaaatgg ctacgagagc tgctctgcaa   540

gctagacgtg ggaagaaaaa atctggttgc cttgtcttgt ga   582

<210> 23
<211> 193
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> RhoA

<400> 23

Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala Cys
1   5   10   15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro Glu
            20   25   30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu Val
            35   40   45

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu
            50   55   60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val Ile
65   70   75   80

Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn Ile Pro
                85   90   95

Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val Pro Ile
                100   105   110

Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Glu His Thr Arg
                115   120   125

Arg Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Glu Glu Gly
            130   135   140

Arg Asp Met Ala Asn Arg Ile Gly Ala Phe Gly Tyr Met Glu Cys Ser
145   150   155   160

Ala Lys Thr Lys Asp Gly Val Arg Glu Val Phe Glu Met Ala Thr Arg
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Ala Ala Leu Gln Ala Arg Arg Gly Lys Lys Lys Ser Gly Cys Leu Val
            180   185   190

Leu

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caagaagatt atgacagatt acgcccccta tcctatccgc aaacagatgt gttcttaatt   240

tgctttttccc ttgtgagtcc tgcatcattt gaaaatgtcc gtgcaaagtg gtatcctgag   300

gtgcggcacc actgtcccaa cactcccatc atcctagtgg gaactaaaact tgatcttagg   360

gatgatdaag acacgatcga gaaactgaag gagaagaagc tgactcccat cacctatccg   420

cagggtctag ccatggctaa ggagattggt gctgtaaaat acctggagtg ctcggcgctc   480

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1   5   10   15

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            20   25   30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Gly .
        35   40   45

Lys Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr
        50   55   60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile
65   70   75   80

Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn Val Arg Ala Lys
                85   90   95

Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Thr Pro Ile Ile Leu
                100   105   110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys
                115   120   125

Leu Lys Glu Lys Lys Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala
            130   135   140

Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser Ala Leu
145   150   155   160

Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val
                165   170   175

Leu Cys Pro Pro Pro Val Lys Lys Arg Lys Arg Lys Cys Leu Leu Leu
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catcaatgtt gcgttgacaa ttggaaaaga aaagtgtaat tgcgtacagg cgaa atg   177
                                                             Met
                                                              1

gca gaa gca aat ccc cgg aga ggc aag atg agg ttc aga agg aat gcg   225
Ala Glu Ala Asn Pro Arg Arg Gly Lys Met Arg Phe Arg Arg Asn Ala
          5   10   15

gct tcc ttc cct ggg aac ttg cac ttg gtt ttg gtt tta cgt cct acc   273
Ala Ser Phe Pro Gly Asn Leu His Leu Val Leu Val Leu Arg Pro Thr
        20   25   30

agc ttt ctt caa cga acg ttc aca gac att gga ttt tgg ttt agt cag   321
Ser Phe Leu Gln Arg Thr Phe Thr Asp Ile Gly Phe Trp Phe Ser Gln
      35   40   45

gag gat ttt atg cct aaa tta cca gtt gtt atg ctg agc tca gtt agt   369
Glu Asp Phe Met Pro Lys Leu Pro Val Val Met Leu Ser Ser Val Ser
50   55   60   65

gat ttg ctg aca tac att gat gac aag caa tta acc cct gag tta ggc   417
Asp Leu Leu Thr Tyr Ile Asp Asp Lys Gln Leu Thr Pro Glu Leu Gly
                70   75   80

ggc acc ttg cag tac tgc cac agt gaa tgg atc atc ttc aga aat gct   465
Gly Thr Leu Gln Tyr Cys His Ser Glu Trp Ile Ile Phe Arg Asn Ala

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             85              90              95

ata gaa aat ttt gcc ctc aca gtg aaa gaa atg gct cag atg tta cag      513
Ile Glu Asn Phe Ala Leu Thr Val Lys Glu Met Ala Gln Met Leu Gln
      100             105             110


tcc ttt gga act gaa ctg gct gag aca gaa cta cca gat gat att ccc      561
Ser Phe Gly Thr Glu Leu Ala Glu Thr Glu Leu Pro Asp Asp Ile Pro
      115             120             125


tca ata gaa gaa att ctg gca att cgt gct gaa agg tat cat ctg ttg      609
Ser Ile Glu Glu Ile Leu Ala Ile Arg Ala Glu Arg Tyr His Leu Leu
130             135             140             145


aag aat gat att aca gct gta acc aaa gaa gga aaa att ctg cta aca      657
Lys Asn Asp Ile Thr Ala Val Thr Lys Glu Gly Lys Ile Leu Leu Thr
              150             155             160


aat ctg gaa gtg cct gac act gaa gga gct gtc agt tca aga cta gaa      705
Asn Leu Glu Val Pro Asp Thr Glu Gly Ala Val Ser Ser Arg Leu Glu
              165             170             175.


tgt cat cgg caa ata agt ggt gac tgg caa act att aat aag ttg ctg      753
Cys His Arg Gln Ile Ser Gly Asp Trp Gln Thr Ile Asn Lys Leu Leu
      180             185             190


act caa gta cat gat atg gaa aca gct ttt gat gga ttt tgg gaa aaa      801
Thr Gln Val His Asp Met Glu Thr Ala Phe Asp Gly Phe Trp Glu Lys
   195             200             205


cat caa tta aaa atg gag cag tat ctg caa cta tgg aag ttt gag cag      849
His Gln Leu Lys Met Glu Gln Tyr Leu Gln Leu Trp Lys Phe Glu Gln
210             215             220             225


gat ttt caa cag ctt gtg act gaa gtt gaa ttt cta tta aac caa caa      897
Asp Phe Gln Gln Leu Val Thr Glu Val Glu Phe Leu Leu Asn Gln Gln
         230             235             240
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gca gaa ctg gct gat gta aca ggg act ata gct caa gta aaa caa aaa   945
Ala Glu Leu Ala Asp Val Thr Gly Thr Ile Ala Gln Val Lys Gln Lys
            245   250   255

ata aaa aaa ttg gaa aac tta gat gaa aat tct cag gag cta tta tca   993
Ile Lys Lys Leu Glu Asn Leu Asp Glu Asn Ser Gln Glu Leu Leu Ser
           260   265   270

aag gcc cag ttt gtg ata tta cat gga cac aag ctt gca gca aat cac   1041
Lys Ala Gln Phe Val Ile Leu His Gly His Lys Leu Ala Ala Asn His
        275   280   285

cat tat gca ctt gat tta atc tgc cag agg tgc aat gag cta cgt tac   1089
His Tyr Ala Leu Asp Leu Ile Cys Gln Arg Cys Asn Glu Leu Arg Tyr
290   295   300   305

ctt tct gat att ttg gtt aat gag ata aaa gca aaa cgg ata caa ctc   1137
Leu Ser Asp Ile Leu Val Asn Glu Ile Lys Ala Lys Arg Ile Gln Leu
            310   315   320

agc agg acc ttc aaa atg cat aaa ctc cta cag cag gct cgt caa tgc   1185
Ser Arg Thr Phe Lys Met His Lys Leu Leu Gln Gln Ala Arg Gln Cys
            325   330   335

tgt gat gaa ggg gaa tgt ctt cta gct aat cag gaa ata gat aag ttt   1233
Cys Asp Glu Gly Glu Cys Leu Leu Ala Asn Gln Glu Ile Asp Lys Phe
            340   345   350

cag tct aaa gaa gat gct cag aaa gct ctc caa gac att gaa aat ttt   1281
Gln Ser Lys Glu Asp Ala Gln Lys Ala Leu Gln Asp Ile Glu Asn Phe
       355   360   365

ctt gaa atg gct cta ccc ttt ata aat tat gaa cct gaa aca ctg cag   1329
Leu Glu Met Ala Leu Pro Phe Ile Asn Tyr Glu Pro Glu Thr Leu Gln
370   375   380   385

tat gaa ttt gat gta ata tta tct cct gag ctt aag gtt caa atg aag   1377
Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met Lys

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                    390                  395                   400

act ata caa ctc aag ctt gaa aac att cga agt ata ttt gag aac cag      1425
Thr Ile Gln Leu Lys Leu Glu Asn Ile Arg Ser Ile Phe Glu Asn Gln
          405                  410                  415

cag gct ggt ttc agg aac ctg gca gat aag cat gtg agg cca atc caa      1473
Gln Ala Gly Phe Arg Asn Leu Ala Asp Lys His Val Arg Pro Ile Gln
          420                  425                  430

ttt gtg gta ccc aca cct gaa aat ttg gtc aca tct ggg aca cca ttt      1521
Phe Val Val Pro Thr Pro Glu Asn Leu Val Thr Ser Gly Thr Pro Phe
        435                  440                  445

ttt tca tct aaa caa ggg aag aag act tgg aga caa aat cag agc aac      1569
Phe Ser Ser Lys Gln Gly Lys Lys Thr Trp Arg Gln Asn Gln Ser Asn
450                  455                  460                  465

tta aaa att gaa gtg gtg cct gat tgt cag gag aag aga agt tct ggt      1617
Leu Lys Ile Glu Val Val Pro Asp Cys Gln Glu Lys Arg Ser Ser Gly
                470                  475                  480

cca tcc tcc agt ttg gac aat ggc aat agc ttg gat gtt tta aag aac      1665
Pro Ser Ser Ser Leu Asp Asn Gly Asn Ser Leu Asp Val Leu Lys Asn
                485                  490                  495

cac gta cta aat gaa ctg ata cag act gag aga gtt tat gtt cga gaa      1713
His Val Leu Asn Glu Leu Ile Gln Thr Glu Arg Val Tyr Val Arg Glu
          500                  505                  510

ctg tat act gtt ttg ttg ggt tat aga gcg gag atg gat aat cca gag      1761
Leu Tyr Thr Val Leu Leu Gly Tyr Arg Ala Glu Met Asp Asn Pro Glu
        515                  520                  525

atg ttt gat ctt atg cca cct ctc ctg aga aat aaa aag gac att ctc      1809
Met Phe Asp Leu Met Pro Pro Leu Leu Arg Asn Lys Lys Asp Ile Leu
530                  535                  540                  545
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ttt gga aac atg gca gaa ata tat gaa ttc cat aac gac att ttc ttg   1857
Phe Gly Asn Met Ala Glu Ile Tyr Glu Phe His Asn Asp Ile Phe Leu
           550   555   560

agc agc ctg gaa aat tgt gct cat gct cca gaa aga gtg gga cct tgt   1905
Ser Ser Leu Glu Asn Cys Ala His Ala Pro Glu Arg Val Gly Pro Cys
           565   570   575

ttc ctg gaa agg aag gat gat ttt cag atg tat gca aaa tat tgt cag   1953
Phe Leu Glu Arg Lys Asp Asp Phe Gln Met Tyr Ala Lys Tyr Cys Gln
          580   585   590

aat aag ccc aga tca gaa aca att tgg agg aag tat tca gaa tgc gca   2001
Asn Lys Pro Arg Ser Glu Thr Ile Trp Arg Lys Tyr Ser Glu Cys Ala
     595   600   605

ttt ttc cag gaa tgt caa aga aag tta aaa cac aga ctt aga ctg gat   2049
Phe Phe Gln Glu Cys Gln Arg Lys Leu Lys His Arg Leu Arg Leu Asp
610   615   620   625

tcc tat tta ctc aaa cca gtg caa cga atc act aaa tat cag tta ttg   2097
Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Thr Lys Tyr Gln Leu Leu
          630   635   640

ttg aag gag cta tta aaa tat agc aaa gac tgt gaa ggt tct gct ctg   2145
Leu Lys Glu Leu Leu Lys Tyr Ser Lys Asp Cys Glu Gly Ser Ala Leu
          645   650   655

ttg aag aag gca ctc gat gca atg ctg gat tta ctg aag tca gtt aat   2193
Leu Lys Lys Ala Leu Asp Ala Met Leu Asp Leu Leu Lys Ser Val Asn
          660   665   670

gat tct atg cat cag att gca ata aat ggc tat att gga aac tta aat   2241
Asp Ser Met His Gln Ile Ala Ile Asn Gly Tyr Ile Gly Asn Leu Asn
     675   680   685

gaa ctg ggc aag atg ata atg caa ggt gga ttc agc gtt tgg ata ggg   2289
Glu Leu Gly Lys Met Ile Met Gln Gly Gly Phe Ser Val Trp Ile Gly

690   695   700   705

cac aag aaa ggt gct aca aaa atg aag gat ttg gct aga ttc aaa cca   2337
His Lys Lys Gly Ala Thr Lys Met Lys Asp Leu Ala Arg Phe Lys Pro
         710   715   720

atg cag cga cac ctt ttc ttg tat gaa aaa gcc att gtt ttt tgc aaa   . 2385
Met Gln Arg His Leu Phe Leu Tyr Glu Lys Ala Ile Val Phe Cys Lys
       725   730   735

agg cgt gtt gaa agt gga gaa ggc tct gac aga tac ccg tca tac agt   2433
Arg Arg Val Glu Ser Gly Glu Gly Ser Asp Arg Tyr Pro Ser Tyr Ser
      740   745   750

ttt aaa cac tgt tgg aaa atg gat gaa gtt gga atc act gaa tat gta   2481
Phe Lys His Cys Trp Lys Met Asp Glu Val Gly Ile Thr Glu Tyr Val
    755   760   765

aaa ggt gat aac cgc aag ttt gaa atc tgg tat ggt gaa aag gaa gaa   2529
Lys Gly Asp Asn Arg Lys Phe Glu Ile Trp Tyr Gly Glu Lys Glu Glu
770   775   780   785

gtt tat att gtc cag gct tct aat gta gat gtg aag atg acg tgg cta   2577
Val Tyr Ile Val Gln Ala Ser Asn Val Asp Val Lys Met Thr Trp Leu
        790   795   800

aaa gaa ata aga aat att ttg ttg aag cag cag gaa ctt ttg aca gtt   2625
Lys Glu Ile Arg Asn Ile Leu Leu Lys Gln Gln Glu Leu Leu Thr Val
       805   810   815

aaa aaa aga aag caa cag gat caa tta aca gaa cgg gat aag ttt cag   2673
Lys Lys Arg Lys Gln Gln Asp Gln Leu Thr Glu Arg Asp Lys Phe Gln
      820   825   830

att tct ctt cag cag aat gat gaa aag caa cag gga gct ttt ata agt   2721
Ile Ser Leu Gln Gln Asn Asp Glu Lys Gln Gln Gly Ala Phe Ile Ser
    835   840   845

act gag gaa act gaa ttg gaa cac acc agc act gtg gtg gag gtc tgt   2769
Thr Glu Glu Thr Glu Leu Glu His Thr Ser Thr Val Val Glu Val Cys
850   855   860   865

gag gca att gcg tca gtt cag gca gaa gca aat aca gtt tgg act gag   2817
Glu Ala Ile Ala Ser Val Gln Ala Glu Ala Asn Thr Val Trp Thr Glu
        870   875   880

gca tca caa tct gca gaa atc tct gaa gaa cct gcg gaa tgg tca agc   2865
Ala Ser Gln Ser Ala Glu Ile Ser Glu Glu Pro Ala Glu Trp Ser Ser
        885   890   895

aac tat ttc tac cct act tat gat gaa aat gaa gaa gaa aat agg ccc   2913
Asn Tyr Phe Tyr Pro Thr Tyr Asp Glu Asn Glu Glu Glu Asn Arg Pro
     900   905   910

ctc atg aga cct gtg tcg gag atg gct ctc cta tat tga tgaagctact   2962
Leu Met Arg Pro Val Ser Glu Met Ala Leu Leu Tyr
    915   920   925

atgtcaaatg gcaagtagct ctttcctgcc tgcttctcag ctcatttgga aaaatactgc   3022

gcaaaagaca ttgagctcaa atgatgcaga tgttgttttc aggttaatgg acacgcaaag   3082

aaaccacagc acatacttct tttctttcat ttaataaagc ttttaattat ggtacgctgt   3142

ctttttaaaa tcatgtattt aatgtgtcag atattgtgct tgaaagattc tcatctcaga   3202

atactttttgg acttgaaaat tatttcttct ctactttgta accaaatgca atcggtgtgc   3262

cttggattat ttagtttatt aatgaattaa gtcaaaatta cggctgcaaa atggctaagg   3322

tcaagtaaag cacaacatta tgatttaata tgctttttgtt gaaaccacag cttttgtgcc   3382

cattgtttta acttgtgtga aacaatacaa agcccagaaa ttctttcgg ggcatgagta   3442

aattttgttc agggctactg tctgtatgtg cccagataaa atttcatga gagtagttta   3502

caaaagccgt atttaaaagt taatattttc acactttttt tctggatttc tgcttataat   3562

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Ala Ala Ser Phe Pro Gly Asn Leu His Leu Val Leu Val Leu Arg Pro
            20   25   30

Thr Ser Phe Leu Gln Arg Thr Phe Thr Asp Ile Gly Phe Trp Phe Ser
            35   40   45

Gln Glu Asp Phe Met Pro Lys Leu Pro Val Val Met Leu Ser Ser Val
        50   55   60

Ser Asp Leu Leu Thr Tyr Ile Asp Asp Lys Gln Leu Thr Pro Glu Leu
65   70   75   80

Gly Gly Thr Leu Gln Tyr Cys His Ser Glu Trp Ile Ile Phe Arg Asn
                85   90   95

Ala Ile Glu Asn Phe Ala Leu Thr Val Lys Glu Met Ala Gln Met Leu
          100   105   110

Gln Ser Phe Gly Thr Glu Leu Ala Glu Thr Glu Leu Pro Asp Asp Ile
          115   120   125

Pro Ser Ile Glu Glu Ile Leu Ala Ile Arg Ala Glu Arg Tyr His Leu
          130   135   140

Leu Lys Asn Asp Ile Thr Ala Val Thr Lys Glu Gly Lys Ile Leu Leu
145   150   155   160

Thr Asn Leu Glu Val Pro Asp Thr Glu Gly Ala Val Ser Ser Arg Leu
          165   170   175

Glu Cys His Arg Gln Ile Ser Gly Asp Trp Gln Thr Ile Asn Lys Leu
          180   185   190

Leu Thr Gln Val His Asp Met Glu Thr Ala Phe Asp Gly Phe Trp Glu
          195   200   205

Lys His Gln Leu Lys Met Glu Gln Tyr Leu Gln Leu Trp Lys Phe Glu
          210   215   220

Gln Asp Phe Gln Gln Leu Val Thr Glu Val Glu Phe Leu Leu Asn Gln
225   230   235   240

Gln Ala Glu Leu Ala Asp Val Thr Gly Thr Ile Ala Gln Val Lys Gln
          245   250   255

Lys Ile Lys Lys Leu Glu Asn Leu Asp Glu Asn Ser Gln Glu Leu Leu
         260   265   270

Ser Lys Ala Gln Phe Val Ile Leu His Gly His Lys Leu Ala Ala Asn
        275   280   285

His His Tyr Ala Leu Asp Leu Ile Cys Gln Arg Cys Asn Glu Leu Arg
        290   295   300

Tyr Leu Ser Asp Ile Leu Val Asn Glu Ile Lys Ala Lys Arg Ile Gln
305   310   315   320

Leu Ser Arg Thr Phe Lys Met His Lys Leu Leu Gln Gln Ala Arg Gln
        325   330   335

Cys Cys Asp Glu Gly Glu Cys Leu Leu Ala Asn Gln Glu Ile Asp Lys
        340   345   350

Phe Gln Ser Lys Glu Asp Ala Gln Lys Ala Leu Gln Asp Ile Glu Asn
        355   360   365

Phe Leu Glu Met Ala Leu Pro Phe Ile Asn Tyr Glu Pro Glu Thr Leu
        370   375   380

Gln Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met
385   390   395   400

Lys Thr Ile Gln Leu Lys Leu Glu Asn Ile Arg Ser Ile Phe Glu Asn
　　　　　　　405　　　　　　　　410　　　　　　　　415

Gln Gln Ala Gly Phe Arg Asn Leu Ala Asp Lys His Val Arg Pro Ile
　　　　　420　　　　　　　　425　　　　　　　430

Gln Phe Val Val Pro Thr Pro Glu Asn Leu Val Thr Ser Gly Thr Pro
　　　　435　　　　　　　　440　　　　　　　445

Phe Phe Ser Ser Lys Gln Gly Lys Lys Thr Trp Arg Gln Asn Gln Ser
　　　450　　　　　　　455　　　　　　　460

Asn Leu Lys Ile Glu Val Val Pro Asp Cys Gln Glu Lys Arg Ser Ser
465　　　　　　　470　　　　　　　475　　　　　　　480

Gly Pro Ser Ser Ser Leu Asp Asn Gly Asn Ser Leu Asp Val Leu Lys
　　　　　　　485　　　　　　　　490　　　　　　　　495

Asn His Val Leu Asn Glu Leu Ile Gln Thr Glu Arg Val Tyr Val Arg
　　　　　　　500　　　　　　　505　　　　　　　510

Glu Leu Tyr Thr Val Leu Leu Gly Tyr Arg Ala Glu Met Asp Asn Pro
　　　　515　　　　　　　520　　　　　　　525

Glu Met Phe Asp Leu Met Pro Pro Leu Leu Arg Asn Lys Lys Asp Ile
　　　530　　　　　　　535　　　　　　　540

Leu Phe Gly Asn Met Ala Glu Ile Tyr Glu Phe His Asn Asp Ile Phe
545　　　　　　　550　　　　　　　555　　　　　　　560

Leu Ser Ser Leu Glu Asn Cys Ala His Ala Pro Glu Arg Val Gly Pro
              565   570   575

Cys Phe Leu Glu Arg Lys Asp Asp Phe Gln Met Tyr Ala Lys Tyr Cys
              580   585   590

Gln Asn Lys Pro Arg Ser Glu Thr Ile Trp Arg Lys Tyr Ser Glu Cys
              595   600   605

Ala Phe Phe Gln Glu Cys Gln Arg Lys Leu Lys His Arg Leu Arg Leu
              610   615   620

Asp Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Thr Lys Tyr Gln Leu
625   630   635   640

Leu Leu Lys Glu Leu Leu Lys Tyr Ser Lys Asp Cys Glu Gly Ser Ala
              645   650   655

Leu Leu Lys Lys Ala Leu Asp Ala Met Leu Asp Leu Leu Lys Ser Val
              660   665   670

Asn Asp Ser Met His Gln Ile Ala Ile Asn Gly Tyr Ile Gly Asn Leu
              675   680   685

Asn Glu Leu Gly Lys Met Ile Met Gln Gly Gly Phe Ser Val Trp Ile
       690   695   700

Gly His Lys Lys Gly Ala Thr Lys Met Lys Asp Leu Ala Arg Phe Lys
705   710   715   720

Pro Met Gln Arg His Leu Phe Leu Tyr Glu Lys Ala Ile Val Phe Cys
              725   730   735

Lys Arg Arg Val Glu Ser Gly Glu Gly Ser Asp Arg Tyr Pro Ser Tyr
              740   745   750

Ser Phe Lys His Cys Trp Lys Met Asp Glu Val Gly Ile Thr Glu Tyr
              755   760   765

Val Lys Gly Asp Asn Arg Lys Phe Glu Ile Trp Tyr Gly Glu Lys Glu
              770   775   780

Glu Val Tyr Ile Val Gln Ala Ser Asn Val Asp Val Lys Met Thr Trp
785   790   795   800

Leu Lys Glu Ile Arg Asn Ile Leu Leu Lys Gln Gln Glu Leu Leu Thr
              805   810   815

Val Lys Lys Arg Lys Gln Gln Asp Gln Leu Thr Glu Arg Asp Lys Phe
              820   825   830

Gln Ile Ser Leu Gln Gln Asn Asp Glu Lys Gln Gln Gly Ala Phe Ile
              835   840   845

Ser Thr Glu Glu Thr Glu Leu Glu His Thr Ser Thr Val Val Glu Val
850   855   860

Cys Glu Ala Ile Ala Ser Val Gln Ala Glu Ala Asn Thr Val Trp Thr
865   870   875   880

Glu Ala Ser Gln Ser Ala Glu Ile Ser Glu Glu Pro Ala Glu Trp Ser
            885   890   895

Ser Asn Tyr Phe Tyr Pro Thr Tyr Asp Glu Asn Glu Glu Glu Asn Arg
         900   905   910

Pro Leu Met Arg Pro Val Ser Glu Met Ala Leu Leu Tyr
        915   920   925